GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 17, 2005, 23:58:38 ; Search time 42 Seconds
(without alignments)
579.419 Million cell updates/sec

Title: SEQ2-129X-307X
Perfect score: 1743
Sequence: 1 ASTKGPSVFPLAPCSRSTSE.....xHEALHNHYTQKSLSLSPSK 326

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1743	100.0	326	2	US-08-656-586-9	Sequence 9, Appli
2	1731	99.3	451	4	US-09-472-087-70	Sequence 70, Appl
3	1731	99.3	463	4	US-09-472-087-1	Sequence 1, Appli
4	1731	99.3	463	4	US-09-472-087-4	Sequence 4, Appli
5	1731	99.3	463	4	US-09-472-087-63	Sequence 63, Appl
6	1731	99.3	463	4	US-09-472-087-68	Sequence 68, Appl
7	1731	99.3	464	4	US-09-472-087-2	Sequence 2, Appli
8	1731	99.3	464	4	US-09-472-087-66	Sequence 66, Appl
9	1731	99.3	470	4	US-09-859-053-28	Sequence 28, Appl
10	1731	99.3	470	4	US-09-859-053-32	Sequence 32, Appl
11	1731	99.3	470	4	US-09-859-053-36	Sequence 36, Appl
12	1731	99.3	530	3	US-08-477-460B-4	Sequence 4, Appli
13	1731	99.3	530	3	US-08-379-516-4	Sequence 4, Appli
14	1731	99.3	530	3	US-09-329-916-4	Sequence 4, Appli
15	1731	99.3	530	3	US-08-485-372A-4	Sequence 4, Appli
16	1731	99.3	530	3	US-09-409-006A-4	Sequence 4, Appli
17	1731	99.3	530	4	US-08-484-681-4	Sequence 4, Appli
18	1731	99.3	530	4	US-09-766-995-4	Sequence 4, Appli
19	1731	99.3	530	5	PCT-US93-07422-4	Sequence 4, Appli
20	1728.5	99.2	462	4	US-09-627-896B-24	Sequence 24, Appl
21	1725	99.0	463	4	US-09-472-087-64	Sequence 64, Appl
22	1720	98.7	450	2	US-08-788-800-12	Sequence 12, Appl
23	1720	98.7	469	2	US-07-934-373C-23	Sequence 23, Appl
24	1720	98.7	469	3	US-08-437-642B-23	Sequence 23, Appl
25	1720	98.7	469	4	US-08-146-206C-23	Sequence 23, Appl
26	1720	98.7	469	4	US-09-705-686-23	Sequence 23, Appl
27	1720	98.7	469	4	US-09-705-392A-23	Sequence 23, Appl
28	1720	98.7	469	4	US-09-705-398-23	Sequence 23, Appl
29	1685	96.7	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	1591.5	91.3	467	3	US-08-523-894-12	Sequence 12, Appl
31	1588	91.1	330	4	US-09-301-593-22	Sequence 22, Appl
32	1588	91.1	450	4	US-09-996-288-208	Sequence 208, App
33	1588	91.1	450	4	US-09-996-288-210	Sequence 210, App
34	1588	91.1	450	4	US-09-996-288-212	Sequence 212, App
35	1588	91.1	450	4	US-09-996-288-214	Sequence 214, App
36	1588	91.1	450	4	US-09-996-288-216	Sequence 216, App
37	1588	91.1	450	4	US-09-996-288-218	Sequence 218, App
38	1588	91.1	450	4	US-09-996-288-220	Sequence 220, App
39	1588	91.1	450	4	US-09-996-288-222	Sequence 222, App
40	1588	91.1	450	4	US-09-996-288-224	Sequence 224, App
41	1588	91.1	450	4	US-09-996-288-226	Sequence 226, App
42	1588	91.1	450	4	US-09-996-288-228	Sequence 228, App
43	1588	91.1	450	4	US-09-996-288-232	Sequence 232, App
44	1588	91.1	450	4	US-09-996-288-234	Sequence 234, App
45	1588	91.1	450	4	US-09-996-288-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-08-656-586-9
; Sequence 9, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Cole, Michael S.
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 326 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..326
; OTHER INFORMATION: /note= "heavy chain constant region of
; OTHER INFORMATION: IgG2 mutant 3"
US-08-656-586-9

Query Match 100.0%; Score 1743; DB 2; Length 326;
Best Local Similarity 99.4%; Pred. No. 3.4e-153;

```
  Matches  324;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||||
Db        301 VFSCSVMHEALHNHYTQKSLSLSPSK 326


RESULT 2
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-70

  Query Match             99.3%;  Score 1731;  DB 4;  Length 451;
  Best Local Similarity   98.5%;  Pred. No. 7.1e-152;
  Matches  321;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 185

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db        186 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF 245

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 305

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 365

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 425

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||||
Db        426 VFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 3
US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-1

  Query Match             99.3%;  Score 1731;  DB 4;  Length 463;
  Best Local Similarity   98.5%;  Pred. No. 7.4e-152;
  Matches  321;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db        198 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF 257

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 317

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 377

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 437

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||||
Db        438 VFSCSVMHEALHNHYTQKSLSLSPGK 463


RESULT 4
US-09-472-087-4
; Sequence 4, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
```

GenCore version 5.1.6

protein - protein search, using sw model

n on: November 17, 2005, 23:47:57 ; Search time 164 Seconds
(without alignments)
768.804 Million cell updates/sec

tle: SEQ2-129X-307X
rfect score: 1743
quence: 1 ASTKGPSVFPLAPCSRSTSE.....xHEALHNHYTQKSLSLSPSK 326

oring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

arched: 2105692 seqs, 386760381 residues

tal number of hits satisfying chosen parameters: 2105692

nimum DB seq length: 0
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1743	100.0	326	8	ADN33229	Adn33229 IgG2M3-CH
2	1738	99.7	326	2	AAW36163	Aaw36163 Heavy cha
3	1731	99.3	326	4	AAE02643	Aae02643 Human imm
4	1731	99.3	326	5	AAM47857	Aam47857 Human Ig-
5	1731	99.3	326	5	ABG30462	Abg30462 Human ant
6	1731	99.3	326	5	ABG77148	Abg77148 Anti-IGF-
7	1731	99.3	326	6	AAE32916	Aae32916 Human imm
8	1731	99.3	326	6	AAE32628	Aae32628 Human imm
9	1731	99.3	326	6	AAO30894	Aao30894 Human imm
10	1731	99.3	326	7	ADE97353	Ade97353 Human IgG
11	1731	99.3	326	7	ADF75002	Adf75002 Human Ig
12	1731	99.3	326	8	ADM41541	Adm41541 Anti-inte
13	1731	99.3	326	8	ADQ95469	Adq95469 Human IgG
14	1731	99.3	326	8	ADR28562	Adr28562 Human ant
15	1731	99.3	443	2	AAY31670	Aay31670 Human IgG
16	1731	99.3	445	8	ADK52332	Adk52332 Human ant
17	1731	99.3	445	8	ADK52384	Adk52384 Human ant
18	1731	99.3	445	8	ADK52296	Adk52296 Human ant
19	1731	99.3	445	8	ADK52312	Adk52312 Human ant
20	1731	99.3	451	3	AAY93734	Aay93734 The heavy
21	1731	99.3	451	6	AAE35889	Aae35889 Human 11.
22	1731	99.3	458	8	ADP07903	Adp07903 Human imm
23	1731	99.3	462	3	AAB26884	Aab26884 Human imm
24	1731	99.3	463	3	AAY93701	Aay93701 The heavy
25	1731	99.3	463	3	AAY93727	Aay93727 The heavy
26	1731	99.3	463	3	AAY93707	Aay93707 The heavy
27	1731	99.3	463	3	AAY93732	Aay93732 The heavy
28	1731	99.3	463	6	AAE35882	Aae35882 Human 4.1
29	1731	99.3	463	6	AAE35887	Aae35887 Human 6.1
30	1731	99.3	463	8	ADM41569	Adm41569 Anti-inte
31	1731	99.3	464	3	AAY93730	Aay93730 The heavy
32	1731	99.3	464	3	AAY93703	Aay93703 The heavy
33	1731	99.3	464	6	AAE35885	Aae35885 Human 4.8
34	1731	99.3	464	7	ADE28411	Ade28411 Human ant
35	1731	99.3	465	7	ADE28459	Ade28459 Human ant
36	1731	99.3	465	8	ADM41557	Adm41557 Anti-inte
37	1731	99.3	465	8	ADM41563	Adm41563 Anti-inte
38	1731	99.3	466	7	ADE28471	Ade28471 Human ant
39	1731	99.3	466	7	ADE28419	Ade28419 Human ant
40	1731	99.3	466	7	ADE28479	Ade28479 Human ant
41	1731	99.3	467	6	ABP71365	Abp71365 Anti-OPGL
42	1731	99.3	469	7	ADE28463	Ade28463 Human ant
43	1731	99.3	470	5	AAU74298	Aau74298 Anti-huma
44	1731	99.3	470	5	AAU74300	Aau74300 Anti-huma
45	1731	99.3	470	5	AAU74296	Aau74296 Anti-huma

ALIGNMENTS

RESULT 1
ADN33229
ID ADN33229 standard; protein; 326 AA.
XX
AC ADN33229;
XX
DT 18-NOV-2004 (first entry)
XX
DE IgG2M3-CH heavy chain constant region.
XX
KW IgG2M3-CH; antibody; IgG; heavy chain constant region;
KW FcRn binding affinity; asthma; autoimmune disease; cancer;
KW viral infection; antiasthmatic; immunosuppressive; cytostatic; virucide.
XX
OS Unidentified.
XX
PN WO2004035752-A2.
XX
PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-US033037.
XX
PR 15-OCT-2002; 2002US-0418972P.
PR 10-APR-2003; 2003US-0462014P.
PR 03-JUN-2003; 2003US-0475762P.
PR 29-AUG-2003; 2003US-0499048P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Hinton PR, Tsurushita N, Tso YJ, Vasquez M;
XX
DR WPI; 2004-348446/32.
XX
PT New modified antibody of class IgG having an altered FcRn binding
PT affinity and/or serum half-life, useful in immunology and protein
PT engineering, and for diagnosing or treating asthma, autoimmune diseases,
PT cancer and viral infections.
XX
PS Disclosure; SEQ ID NO 2; 140pp; English.
XX
CC The invention relates to a modified antibody of class IgG where at least
CC one amino acid residue from the heavy chain constant region is different
CC from that present in an unmodified class IgG antibody, and where the FcRn
CC binding affinity and/or serum half-life of the modified antibody is
CC altered relative to that of the unmodified antibody. The methods and
CC compositions of the present invention are useful in the fields of
CC immunology and protein engineering, in particular for using modified
CC class IgG antibodies for diagnosing and treating asthma, autoimmune

diseases, cancer and viral infections. This sequence represents the antibody IgG2M3-CH heavy chain constant region of the invention.

Sequence 326 AA;

```
Query Match             100.0%;  Score 1743;  DB 8;  Length 326;
Best Local Similarity   99.4%;  Pred. No. 4.2e-126;
Matches  324;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
            ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
            ||||||:||||||||||||||||||||
        301 VFSCSVMHEALHNHYTQKSLSLSPSK 326
```

ESULT 2
W36163
AAW36163 standard; protein; 326 AA.

AAW36163;

22-MAY-1998 (first entry)

Heavy chain constant region of IgG2 mutant 3.

Mutant; immunoglobulin G2; IgG2; heavy chain; constant region; low mitogenic response; human T-cell; immunosuppressant; diagnosis; immune system disease.

Homo sapiens.
Synthetic.

WO9744362-A1.

27-NOV-1997.

19-MAY-1997; 97WO-US008576.

20-MAY-1996; 96US-00650410.
31-MAY-1996; 96US-00656586.

(PROT-) PROTEIN DESIGN LABS INC.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.

Tso JY, Cole MS, Anasetti C;

WPI; 1998-018436/02.

Mutated immunoglobulin G 2 constant region that does not induce T cell proliferation - and anti-CD3 antibodies containing this region for use as immunosuppressant with reduced side effects.

Claim 6; Fig 4; 63pp; English.

CC The present sequence was used in the development of a novel mutated
CC immunoglobulin G (IgG) 2 constant region (CR), having a non-natural
CC segment of amino acids between 234 and 237 (EU numbering system), so that
CC an antibody (Ab) containing the variable region of an anti-CD3 Ab linked
CC to the CR induces lower mitogenic response in human T-cells than does a
CC similar Ab containing the natural IgG2 constant region. The Ab are useful
CC as immunosuppressants, e.g. in autoimmune disease (including rheumatoid
CC arthritis, multiple sclerosis, type I diabetes, systemic lupus
CC erythematosus and inflammatory bowel disease), transplant rejection,
CC graft versus host disease, inflammation allergy or sepsis, particularly
CC acute episodes of autoimmune diseases. The Ab can also be used for
CC diagnosis of immune system disease and for determining T cell numbers in
CC patients with acquired immune deficiency syndrome (AIDS). The Ab have
CC fewer side effects than known anti-CD3 Ab, as they do not, in most
CC patients, induce mitogenesis through specific binding to Fc gamma
CC receptors, nor release of cytokines. Compared with F(ab')2 fragments, the
CC Ab have a longer half-life
XX
SQ Sequence 326 AA;

```
  Query Match             99.7%;  Score 1738;  DB 2;  Length 326;
  Best Local Similarity   99.1%;  Pred. No. 1e-125;
  Matches  323;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSNFGTQTWTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||||||
Db        301 VFSCSVMHEALHNHYTQKSLSLSPSK 326
```

RESULT 3
AAE02643
ID AAE02643 standard; protein; 326 AA.
XX
AC AAE02643;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human immunoglobulin G2 constant region mature protein.
XX
KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
KW vaccine; haemostatic; immunoglobulin G2; IgG2; EPO deficient disease;
KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
KW haematopoietic growth factor.
XX
OS Homo sapiens.
XX
PN WO200136489-A2.
XX
PD 25-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-EP010843.
XX
PR 12-NOV-1999; 99US-0164855P.

GenCore version 5.1.6

protein - protein search, using sw model

on: November 18, 2005, 00:07:19 ; Search time 164 Seconds
(without alignments)
831.716 Million cell updates/sec

le: SEQ2-129X-307X
fect score: 1743
uence: 1 ASTKGPSVFPLAPCSRSTSE.....xHEALHNHYTQKSLSLSPSK 326

ring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

rched: 1867879 seqs, 418409474 residues

al number of hits satisfying chosen parameters: 1867879

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	1743	100.0	326	17	US-10-822-300-2	Sequence 2, Appli
2	1743	100.0	326	17	US-10-822-300-10	Sequence 10, Appl
3	1743	100.0	326	17	US-10-822-300-11	Sequence 11, Appl
4	1743	100.0	326	17	US-10-822-300-12	Sequence 12, Appl
5	1743	100.0	326	17	US-10-822-300-13	Sequence 13, Appl
6	1743	100.0	326	17	US-10-822-300-14	Sequence 14, Appl
7	1743	100.0	326	17	US-10-822-300-15	Sequence 15, Appl
8	1743	100.0	326	17	US-10-822-300-16	Sequence 16, Appl
9	1743	100.0	326	17	US-10-822-300-17	Sequence 17, Appl
10	1743	100.0	326	17	US-10-822-300-18	Sequence 18, Appl
11	1743	100.0	326	17	US-10-822-300-19	Sequence 19, Appl
12	1743	100.0	326	17	US-10-822-300-20	Sequence 20, Appl
13	1743	100.0	326	17	US-10-822-300-21	Sequence 21, Appl
14	1743	100.0	326	17	US-10-822-300-22	Sequence 22, Appl
15	1743	100.0	326	17	US-10-822-300-23	Sequence 23, Appl
16	1743	100.0	326	17	US-10-822-300-24	Sequence 24, Appl
17	1743	100.0	326	17	US-10-822-300-25	Sequence 25, Appl
18	1743	100.0	326	17	US-10-822-300-26	Sequence 26, Appl
19	1743	100.0	326	17	US-10-822-300-27	Sequence 27, Appl
20	1743	100.0	326	17	US-10-822-300-28	Sequence 28, Appl
21	1743	100.0	326	17	US-10-822-300-48	Sequence 48, Appl
22	1743	100.0	326	17	US-10-822-300-49	Sequence 49, Appl
23	1743	100.0	326	17	US-10-822-300-50	Sequence 50, Appl
24	1743	100.0	326	17	US-10-822-300-51	Sequence 51, Appl
25	1743	100.0	326	17	US-10-822-300-52	Sequence 52, Appl
26	1743	100.0	326	17	US-10-822-300-53	Sequence 53, Appl
27	1743	100.0	326	17	US-10-822-300-54	Sequence 54, Appl
28	1743	100.0	326	17	US-10-822-300-55	Sequence 55, Appl
29	1743	100.0	326	17	US-10-822-300-56	Sequence 56, Appl
30	1743	100.0	326	17	US-10-822-300-57	Sequence 57, Appl
31	1743	100.0	326	17	US-10-822-300-58	Sequence 58, Appl
32	1743	100.0	326	17	US-10-822-300-59	Sequence 59, Appl
33	1743	100.0	326	17	US-10-822-300-60	Sequence 60, Appl
34	1743	100.0	326	17	US-10-822-300-61	Sequence 61, Appl
35	1743	100.0	326	17	US-10-822-300-62	Sequence 62, Appl
36	1743	100.0	326	17	US-10-822-300-63	Sequence 63, Appl
37	1743	100.0	326	17	US-10-822-300-64	Sequence 64, Appl
38	1743	100.0	326	17	US-10-822-300-65	Sequence 65, Appl
39	1743	100.0	326	17	US-10-822-300-66	Sequence 66, Appl
40	1743	100.0	326	17	US-10-822-300-72	Sequence 72, Appl
41	1743	100.0	326	17	US-10-822-300-73	Sequence 73, Appl
42	1743	100.0	326	17	US-10-822-300-74	Sequence 74, Appl
43	1743	100.0	326	17	US-10-687-118-2	Sequence 2, Appli
44	1743	100.0	326	17	US-10-687-118-10	Sequence 10, Appl
45	1743	100.0	326	17	US-10-687-118-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-822-300-2
; Sequence 2, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-2

Query Match 100.0%; Score 1743; DB 17; Length 326;
Best Local Similarity 99.4%; Pred. No. 6.7e-127;
Matches 324; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
```

```
       181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

       241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

       301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
           ||||||:||||||||||||||||||||
       301 VFSCSVMHEALHNHYTQKSLSLSPSK 326


ULT 2
10-822-300-10
equence 10, Application US/10822300
ublication No. US20050014934A1
ENERAL INFORMATION:
APPLICANT: Hinton, et al.
TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION:  ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.CPUS01
CURRENT APPLICATION NUMBER: US/10/822,300
CURRENT FILING DATE:  2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
EQ ID NO 10
 LENGTH: 326
 TYPE: PRT
 ORGANISM: Homo sapiens
10-822-300-10

uery Match             100.0%;  Score 1743;  DB 17;  Length 326;
est Local Similarity   99.4%;  Pred. No. 6.7e-127;
atches  324;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

         1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

        61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

       121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
           |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
       121 LFPPKPKDALMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

       181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

       241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

       301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
           ||||||:||||||||||||||||||||
       301 VFSCSVMHEALHNHYTQKSLSLSPSK 326


ULT 3
10-822-300-11
equence 11, Application US/10822300
ublication No. US20050014934A1
ENERAL INFORMATION:
APPLICANT: Hinton, et al.
TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
TITLE OF INVENTION:  ANTIBODIES BY MUTAGENESIS
FILE REFERENCE: 05882.0039.CPUS01
CURRENT APPLICATION NUMBER: US/10/822,300
CURRENT FILING DATE:  2004-04-09

;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-822-300-11

  Query Match             100.0%;  Score 1743;  DB 17;  Length 326;
  Best Local Similarity   99.4%;  Pred. No. 6.7e-127;
  Matches  324;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDCLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||||||
Db        301 VFSCSVMHEALHNHYTQKSLSLSPSK 326


RESULT 4
US-10-822-300-12
; Sequence 12, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
;  APPLICANT: Hinton, et al.
;  TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
;  TITLE OF INVENTION:  ANTIBODIES BY MUTAGENESIS
;  FILE REFERENCE: 05882.0039.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/822,300
;  CURRENT FILING DATE:  2004-04-09
;  NUMBER OF SEQ ID NOS: 146
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 326
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-822-300-12

  Query Match             100.0%;  Score 1743;  DB 17;  Length 326;
  Best Local Similarity   99.4%;  Pred. No. 6.7e-127;
  Matches  324;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDDLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
```

GenCore version 5.1.6

protein - protein search, using sw model

on: November 17, 2005, 23:56:58 ; Search time 40 Seconds
(without alignments)
784.167 Million cell updates/sec

le: SEQ2-129X-307X
fect score: 1743
uence: 1 ASTKGPSVFPLAPCSRSTSE.....xHEALHNHYTQKSLSLSPSK 326

ring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

rched: 283416 seqs, 96216763 residues

al number of hits satisfying chosen parameters: 283416

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	1731	99.3	326	1	G2HU	Ig gamma-2 chain C
2	1583.5	90.8	327	1	G4HU	Ig gamma-4 chain C
3	1582	90.8	330	1	GHHU	Ig gamma-1 chain C
4	1558.5	89.4	377	2	A23511	Ig gamma-3 chain C
5	1549.5	88.9	377	2	A60764	Ig gamma-3 chain C
6	1254	71.9	328	2	I47159	Ig gamma 2a chain
7	1248	71.6	328	2	I47160	Ig gamma 2b chain
8	1222	70.1	328	2	I47161	Ig gamma 3 chain c
9	1212	69.5	328	2	I47158	Ig gamma 1 chain c
10	1185.5	68.0	323	1	GHRB	Ig gamma chain C r
11	1178.5	67.6	472	2	S31459	Ig gamma-1 chain -
12	1164	66.8	326	2	PS0017	Ig gamma-1 chain C
13	1162.5	66.7	470	2	S22080	Ig heavy chain pre
14	1156	66.3	444	2	PC4436	monoclonal antibod
15	1150.5	66.0	329	1	G2GP	Ig gamma-2 chain C
16	1140	65.4	324	1	G1MS	Ig gamma-1 chain C
17	1135	65.1	393	1	G1MSM	Ig gamma-1 chain C
18	1134.5	65.1	374	2	S69339	Ig heavy chain V r
19	1129	64.8	255	4	S31866	Ig gamma-1 chain C
20	1126.5	64.6	308	2	C30554	Ig heavy chain C r
21	1120	64.3	322	2	PS0019	Ig gamma-2a chain
22	1118	64.1	234	2	PT0207	Ig gamma chain C r
23	1108.5	63.6	333	2	PS0018	Ig gamma-2b chain
24	1107.5	63.5	329	2	S00847	Ig gamma-2c chain
25	1100.5	63.1	327	2	S06611	Ig gamma-2 chain C
26	1096	62.9	289	1	G3HUWI	Ig gamma-3 heavy c
27	1085	62.2	329	1	G3MSC	Ig gamma-3 chain C
28	1082	62.1	330	1	G2MSA	Ig gamma-2a chain
29	1082	62.1	469	2	S37483	Ig gamma-2a chain
30	1080	62.0	398	1	G3MSM	Ig gamma-3 chain C
31	1077.5	61.8	335	1	G2MSAB	Ig gamma-2a chain
32	1077	61.8	399	1	G2MSAM	Ig gamma-2a chain
33	1067	61.2	446	2	S40295	Ig gamma-2a chain
34	1051	60.3	277	2	I47162	Ig gamma 4 chain c
35	1043	59.8	405	1	G2MSBM	Ig gamma-2b chain
36	1026	58.9	475	2	S01321	Ig gamma-2b chain
37	1025.5	58.8	474	1	G2MS11	Ig gamma-2b chain
38	696	39.9	180	2	I46732	Ig gamma heavy cha
39	673.5	38.6	548	2	S38864	Ig epsilon chain C
40	639	36.7	241	2	S69131	Ig heavy chain (DO
41	574	32.9	152	2	S14236	Ig gamma-1 chain C
42	567	32.5	249	2	S69340	Ig heavy chain VHI
43	561	32.2	549	2	S04845	Ig heavy chain pre
44	554	31.8	218	2	A36040	Ig heavy chain V-I
45	519.5	29.8	448	2	S03186	Ig heavy chain C r

ALIGNMENTS

RESULT 1
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PI
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fu
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a h
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-2
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ga
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds

```
rangione, B.; Milstein, C.; Pink, J.R.L.
ure 221, 145-148, 1969
itle: Structural studies of immunoglobulin G.
eference number: A93157; MUID:69064124; PMID:5782707
ontents: annotation; Sa, disulfide bonds
enetics:
ene: GDB:IGHG2
ross-references: GDB:119338; OMIM:147110
ap position: 14q32.33-14q32.33
omplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
n disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
uperfamily: immunoglobulin C region; immunoglobulin homology
eywords: duplication; glycoprotein; heterotetramer; immunoglobulin
0-85/Domain: immunoglobulin homology <IM1>
33-202/Domain: immunoglobulin homology <IM2>
39-306/Domain: immunoglobulin homology <IM3>
4/Disulfide bonds: interchain (to light chain) #status experimental
7-83,140-200,246-304/Disulfide bonds: #status experimental
02,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
76/Binding site: carbohydrate (Asn) (covalent) #status predicted

uery Match             99.3%;  Score 1731;  DB 1;  Length 326;
est Local Similarity   98.5%;  Pred. No. 1.2e-112;
atches  321;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF 120

        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
            ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
            ||||||:||||||||||||||||| |
        301 VFSCSVMHEALHNHYTQKSLSLSPGK 326


ULT 2
U
gamma-4 chain C region - human
pecies: Homo sapiens (man)
ate: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
ccession: A90933; A90249; A02150
llison, J.; Buxbaum, J.; Hood, L.
 1, 11-18, 1981
itle: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
eference number: A90933; MUID:83157104; PMID:6299662
ccession: A90933
olecule type: DNA
esidues: 1-327 <ELL>
ross-references: UNIPROT:P01861
ote: the sequence was determined from the germline gene
ink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
chem. J. 117, 33-47, 1970
itle: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
eference number: A90249; MUID:70207560; PMID:4192699
ccession: A90249
olecule type: protein
esidues: 1-30;81-326 <PIN>
enetics:
```

```
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             90.8%;  Score 1583.5;  DB 1;  Length 327;
  Best Local Similarity   91.1%;  Pred. No. 2e-102;
  Matches  298;  Conservative   11;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP-AAAPSV 119
              |||||||||||||: ||:|||||||||||||||| || |    || ||||     |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120

Qy        120 FLFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF 179
              |||||||||:|||||||||||||||| ||||||||||||||||||||||||||||||||:
Db        121 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 180

Qy        180 RVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTK 239
              |||||||:|||||||||||||||||||: ||||||| |||||||||||||||:|||||
Db        181 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 240

Qy        240 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQG 299
              |||||||||||||||||||||||||||||||||:||||||||||:|||||||||:|
Db        241 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 300

Qy        300 NVFSCSVXHEALHNHYTQKSLSLSPSK 326
              |||||||:|||||||||||||||  |
Db        301 NVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 3
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a 
A;Reference number: S33887; MUID:83001943; PMID:6811139
```

GenCore version 5.1.6

protein - protein search, using sw model

on: November 17, 2005, 23:56:13 ; Search time 174 Seconds
(without alignments)
959.413 Million cell updates/sec

le: SEQ2-129X-307X
fect score: 1743
uence: 1 ASTKGPSVFPLAPCSRSTSE.....xHEALHNHYTQKSLSLSPSK 326

ring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

rched: 1612378 seqs, 512079187 residues

al number of hits satisfying chosen parameters: 1612378

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	% Query Match	Length	DB	ID	Description
1	1731	99.3	326	1	GC2_HUMAN	P01859 homo sapien
2	1731	99.3	417	2	Q6N093	Q6n093 homo sapien
3	1726	99.0	465	2	Q6P6C4	Q6p6c4 homo sapien
4	1717	98.5	493	2	Q68CN4	Q68cn4 homo sapien
5	1716	98.5	464	2	Q6MZU6	Q6mzu6 homo sapien
6	1588	91.1	348	2	Q6PYX1	Q6pyx1 homo sapien
7	1588	91.1	478	2	Q6PI81	Q6pi81 homo sapien
8	1588	91.1	480	2	Q6PJF1	Q6pjf1 homo sapien
9	1583.5	90.8	327	1	GC4_HUMAN	P01861 homo sapien
10	1583.5	90.8	473	2	Q8TC63	Q8tc63 homo sapien
11	1582	90.8	330	1	GC1_HUMAN	P01857 homo sapien
12	1582	90.8	465	2	Q6GMX6	Q6gmx6 homo sapien
13	1582	90.8	466	2	Q6IN78	Q6in78 homo sapien
14	1582	90.8	469	2	Q7Z7P5	Q7z7p5 homo sapien
15	1582	90.8	470	2	Q6PJA4	Q6pja4 homo sapien
16	1582	90.8	470	2	Q7Z5W1	Q7z5w1 homo sapien
17	1582	90.8	472	2	Q6N089	Q6n089 homo sapien
18	1582	90.8	475	2	Q6GMW7	Q6gmw7 homo sapien
19	1582	90.8	476	2	Q6GMX1	Q6gmx1 homo sapien
20	1580.5	90.7	476	2	Q6MZX7	Q6mzx7 homo sapien
21	1578	90.5	473	2	Q6MZV7	Q6mzv7 homo sapien
22	1578	90.5	473	2	Q6P055	Q6p055 homo sapien
23	1578	90.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
24	1578	90.5	480	2	Q6N094	Q6n094 homo sapien
25	1578	90.5	481	2	Q6N097	Q6n097 homo sapien
26	1578	90.5	482	2	Q7Z351	Q7z351 homo sapien
27	1577	90.5	544	2	Q6PJ95	Q6pj95 homo sapien
28	1575	90.4	466	2	Q6N096	Q6n096 homo sapien
29	1571	90.1	475	2	Q6N095	Q6n095 homo sapien
30	1561.5	89.6	521	2	Q8N4Y9	Q8n4y9 homo sapien
31	1558.5	89.4	518	2	Q6N030	Q6n030 homo sapien
32	1556.5	89.3	509	2	Q8NF17	Q8nf17 homo sapien
33	1453.5	83.4	354	2	Q86TT2	Q86tt2 homo sapien
34	1193.5	68.5	337	2	Q95M34	Q95m34 equus cabal
35	1185.5	68.0	323	1	GC_RABIT	P01870 oryctolagus
36	1164	66.8	326	1	GC1_RAT	P20759 rattus norv
37	1157	66.4	463	2	Q99LC4	Q99lc4 mus musculu
38	1156	66.3	458	2	Q65ZQ1	Q65zq1 homo sapien
39	1150.5	66.0	329	1	GC2_CAVPO	P01862 cavia porce
40	1140	65.4	324	1	GC1_MOUSE	P01868 mus musculu
41	1135	65.1	393	1	GC1M_MOUSE	P01869 mus musculu
42	1126	64.6	487	2	Q65ZL2	Q65zl2 mus sp. fv/
43	1125	64.5	679	2	Q96PQ8	Q96pq8 homo sapien
44	1120	64.3	322	1	GCA_RAT	P20760 rattus norv
45	1108.5	63.6	333	1	GCB_RAT	P20761 rattus norv

ALIGNMENTS

```
RESULT 1
GC2_HUMAN
ID   GC2_HUMAN      STANDARD;      PRT;   326 AA.
AC   P01859;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig gamma-2 chain C region.
GN   Name=IGHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 2-326 FROM N.A.
RX   MEDLINE=82197621; PubMed=6804948;
RA   Ellison J.W., Hood L.E.;
RT   "Linkage and sequence homology of two human immunoglobulin gamma heavy
RT   chain constant region genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN   [2]
RP   SEQUENCE OF 88-115 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=83001943; PubMed=6811139; DOI=10.1016/0092-8674(82)90183-0;
RA   Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT   "Structure of human immunoglobulin gamma genes: implications for
RT   evolution of a gene family.";
RL   Cell 29:671-679(1982).
RN   [3]
RP   SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=84235992; PubMed=6329676;
RA   Krawinkel U., Rabbitts T.H.;
RT   "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT   heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT   genes.";
RL   EMBO J. 1:403-407(1982).
RN   [4]
RP   SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX   MEDLINE=81007873; PubMed=6774012;
RA   Wang A.-C., Tung E., Fudenberg H.H.;
RT   "The primary structure of a human IgG2 heavy chain: genetic,
RT   evolutionary, and functional implications.";
RL   J. Immunol. 125:1048-1054(1980).
RN   [5]
RP   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX   MEDLINE=80001357; PubMed=113060;
RA   Connell G.E., Parr D.M., Hofmann T.;
RT   "The amino acid sequences of the three heavy chain constant region
RT   domains of a human IgG2 myeloma protein.";
RL   Can. J. Biochem. 57:758-767(1979).
RN   [6]
RP   SEQUENCE OF 238-275 (ZIE).
RX   MEDLINE=80114419; PubMed=118920; DOI=10.1016/0161-5890(79)90091-9;
```

```
Hofmann T., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
[7]
REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
Hofmann T., Parr D.M.;
Submitted (MAR-1980) to the PIR data bank.
[8]
SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
"Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995).
[9]
DISULFIDE BONDS.
MEDLINE=72033500; PubMed=4940472;
Milstein C., Frangione B.;
"Disulphide bridges of the heavy chain of human immunoglobulin G2.";
Biochem. J. 121:217-225(1971).
[10]
DISULFIDE BONDS.
MEDLINE=69064124; PubMed=5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
---
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
---
EMBL; J00230; AAB59393.1; -.
PIR; A93906; G2HU.
HSSP; P01857; 1OQX.
Genew; HGNC:5526; IGHG2.
MIM; 147110; -.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
Direct protein sequencing; Immunoglobulin C region;
Immunoglobulin domain.
NON_TER       1      1
DOMAIN        1     98       CH1.
DOMAIN       99    110       Hinge.
DOMAIN      111    219       CH2.
DOMAIN      220    326       CH3.
DISULFID     14     14       Interchain (with a light chain).
DISULFID     27     83
DISULFID    102    102       Interchain (with a heavy chain).
DISULFID    103    103       Interchain (with a heavy chain).
DISULFID    106    106       Interchain (with a heavy chain).
DISULFID    109    109       Interchain (with a heavy chain).
DISULFID    140    200
DISULFID    246    304
SITE        156    156       At or near the complement-binding site.
VARIANT      60     60       S -> A (in myeloma proteins TIL and ZIE).
                             /FTId=VAR_003889.
CONFLICT    109    109       C -> S (in Ref. 3).
SEQUENCE   326 AA;  35884 MW;  8310878C6878CF9C CRC64;

Query Match             99.3%;  Score 1731;  DB 1;  Length 326;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-116;
  Matches  321;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPAAAPSVF 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVF 120

Qy        121 LFPPKPKDXLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR 180

Qy        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN 240

Qy        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN 300

Qy        301 VFSCSVXHEALHNHYTQKSLSLSPSK 326
              ||||||:||||||||||||||||| |
Db        301 VFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 2
Q6N093
ID   Q6N093      PRELIMINARY;      PRT;   417 AA.
AC   Q6N093;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I04196 (Fragment).
GN   Name=DKFZp686I04196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640623; CAE45777.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   417 AA;  46061 MW;  C4518E844CFB883C CRC64;

  Query Match             99.3%;  Score 1731;  DB 2;  Length 417;
  Best Local Similarity   98.5%;  Pred. No. 1.6e-116;
  Matches  321;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 151
```